



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/737,146

DATE: 08/27/2004

TIME: 16:51:22

Input Set : N:\Crf3\RULE60\10737146.raw

Output Set: N:\CRF4\08272004\J737146.raw

1 <110> APPLICANT: Sims, John
 2 Born, Theresa
 3 <120> TITLE OF INVENTION: ACPL DNA and Polypeptides
 4 <130> FILE REFERENCE: 2872-US
 5 <140> CURRENT APPLICATION NUMBER: US/10/737,146
 6 <141> CURRENT FILING DATE: 2003-12-15
 7 <150> PRIOR APPLICATION NUMBER: US/09/616,530
 8 <151> PRIOR FILING DATE: 2000-07-14
 9 <150> PRIOR APPLICATION NUMBER: PCT/US99/01420
 10 <151> PRIOR FILING DATE: 1999-01-22
 11 <150> PRIOR APPLICATION NUMBER: 60/078,835
 12 <151> PRIOR FILING DATE: 1998-03-20
 13 <150> PRIOR APPLICATION NUMBER: 60/072,301
 14 <151> PRIOR FILING DATE: 1998-01-23
 15 <160> NUMBER OF SEQ ID NOS: 7
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1845
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Mus sp.
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(1845)
 25 <223> OTHER INFORMATION:

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 28 Met Leu Cys Leu Gly Trp Val Phe Leu Trp Phe Val Ala Gly Glu Lys
 29 1 5 10 15
 30 acc aca gga ttt aat cat tca gct tgt gcc acc aaa aaa ctt ctg tgg 96
 31 Thr Thr Gly Phe Asn His Ser Ala Cys Ala Thr Lys Lys Leu Leu Trp
 32 20 25 30
 33 aca tat tct gca agg ggt gca gag aat ttt gtc cta ttt tgt gac tta 144
 34 Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu
 35 35 40 45
 36 caa gag ctt cag gag caa aaa ttc tcc cat gca agt caa ctg tca cca 192
 37 Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro
 38 50 55 60
 39 aca caa agt cct gct cac aaa cct tgc agt ggc agt cag aag gac cta 240
 40 Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu
 41 65 70 75 80
 42 tct gat gtc cag tgg tac atg caa cct cgg agt gga agt cca cta gag 288
 43 Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu
 44 85 90 95

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45	gag atc agt aga aac tct ccc cat atg cag agt gaa ggc atg ctg cat	336
46	Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His	
47	100 105 110	
48	ata ttg gcc cca cag acg aac agc att tgg tca tat att tgt aga ccc	384
49	Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro	
50	115 120 125	
51	aga att agg agc ccc cag gat atg gcc tgt tgt atc aag aca gtc tta	432
52	Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu	
53	130 135 140	
54	gaa gtt aag cct cag aga aac gtg tcc tgt ggg aac aca gca caa gat	480
55	Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp	
56	145 150 155 160	
57	gaa caa gtc cta ctt ctt ggc agt act ggc tcc att cat tgt ccc agt	528
58	Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser	
59	165 170 175	
60	ctc agc tgc caa agt gat gta cag agt cca gag atg acc tgg tac aag	576
61	Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys	
62	180 185 190	
63	gat gga aga cta ctt cct gag cac aag aaa aat cca att gag atg gca	624
64	Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala	
65	195 200 205	
66	gat att tat gtt ttt aat caa ggc ttg tat gta tgt gat tac aca cag	672
67	Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln	
68	210 215 220	
69	tca gat aat gtg agt tcc tgg aca gtc cga gct gtg gtt aaa gtg aga	720
70	Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg	
71	225 230 235 240	
72	acc att ggt aag gac atc aat gtg aag ccg gaa att ctg gat ccc att	768
73	Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile	
74	245 250 255	
75	aca gat aca ctg gac gta gag ctt gga aag cct tta act ctc ccc tgc	816
76	Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys	
77	260 265 270	
78	aga gta cag ttt ggc ttc caa aga ctt tca aag cct gtg ata aag tgg	864
79	Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp	
80	275 280 285	
81	tat gtc aaa gaa tct aca cag gag tgg gaa atg tca gta ttt gag gag	912
82	Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu	
83	290 295 300	
84	aaa aga att caa tcc act ttc aag aat gaa gtc att gaa cgt acc atc	960
85	Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile	
86	305 310 315 320	
87	ttc ttg aga gaa gtt acc cag aga gat ctc agc aga aag ttt gtt tgc	1008
88	Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys	
89	325 330 335	
90	ttt gcc cag aac tcc att ggg aac aca aca cgg acc ata cgg ctg agg	1056
91	Phe Ala Gln Asn Ser Ile Gly Asn Thr Thr Arg Thr Ile Arg Leu Arg	
92	340 345 350	
93	aag aag gaa gag gtg gtg ttt gta tac atc ctt ctc ggc acg gcc ttg	1104

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94	Lys Lys Glu Glu Val Val Phe Val Tyr Ile Leu Leu Gly Thr Ala Leu	
95	355 360 365	
96	atg ctg gtg ggc gtt ctg gtg gca gct gct ttc ctc tac tgg tac tgg	1152
97	Met Leu Val Gly Val Leu Val Ala Ala Ala Phe Leu Tyr Trp Tyr Trp	
98	370 375 380	
99	att gaa gtt gtc ctg ctc tgt cga acc tac aag aac aaa gat gag act	1200
100	Ile Glu Val Val Leu Leu Cys Arg Thr Tyr Lys Asn Lys Asp Glu Thr	
101	385 390 395 400	
102	ctg ggg gat aag aag gaa ttc gat gca ttt gta tcc tac tcg aat tgg	1248
103	Leu Gly Asp Lys Lys Glu Phe Asp Ala Phe Val Ser Tyr Ser Asn Trp	
104	405 410 415	
105	agc tct cct gag act gac gcc gtg gga tct ctg agt gag gaa cac ctg	1296
106	Ser Ser Pro Glu Thr Asp Ala Val Gly Ser Leu Ser Glu Glu His Leu	
107	420 425 430	
108	gct ctg aat ctt ttc ccg gaa gtg cta gaa gac acc tat ggg tac aga	1344
109	Ala Leu Asn Leu Phe Pro Glu Val Leu Glu Asp Thr Tyr Gly Tyr Arg	
110	435 440 445	
111	ttg tgt ttg ctt gac cga gat gtg acc cca gga gga gtg tat gca gat	1392
112	Leu Cys Leu Leu Asp Arg Asp Val Thr Pro Gly Gly Val Tyr Ala Asp	
113	450 455 460	
114	gac att gtg agc atc att aag aaa agc cga aga gga ata ttt atc ctg	1440
115	Asp Ile Val Ser Ile Ile Lys Lys Ser Arg Arg Gly Ile Phe Ile Leu	
116	465 470 475 480	
117	agt ccc agc tac ctc aat gga ccc cgt gtc ttt gag cta caa gca gca	1488
118	Ser Pro Ser Tyr Leu Asn Gly Pro Arg Val Phe Glu Leu Gln Ala Ala	
119	485 490 495	
120	gtg aat ctt gcc ttg gtt gat cag aca ctg aag ttg att tta att aag	1536
121	Val Asn Leu Ala Leu Val Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys	
122	500 505 510	
123	ttc tgt tcc ttc caa gag cca gaa tct ctt cct tac ctt gtc aaa aag	1584
124	Phe Cys Ser Phe Gln Glu Pro Glu Ser Leu Pro Tyr Leu Val Lys Lys	
125	515 520 525	
126	gct ctg cgg gtt ctc ccc aca gtc aca tgg aaa ggc ttg aag tcg gtc	1632
127	Ala Leu Arg Val Leu Pro Thr Val Thr Trp Lys Gly Leu Lys Ser Val	
128	530 535 540	
129	cac gcc agt tcc agg ttc tgg acc caa att cgt tac cac atg cct gtg	1680
130	His Ala Ser Ser Arg Phe Trp Thr Gln Ile Arg Tyr His Met Pro Val	
131	545 550 555 560	
132	aag aac tcc aac agg ttt atg ttc aac ggg ctc aga att ttc ctg aag	1728
133	Lys Asn Ser Asn Arg Phe Met Phe Asn Gly Leu Arg Ile Phe Leu Lys	
134	565 570 575	
135	ggc ttt tcc cct gaa aag gac cta gtg aca cag aaa ccc ctg gaa gga	1776
136	Gly Phe Ser Pro Glu Lys Asp Leu Val Thr Gln Lys Pro Leu Glu Gly	
137	580 585 590	
138	atg ccc aag tct ggg aat gac cac gga gct cag aac ctc ctt ctc tac	1824
139	Met Pro Lys Ser Gly Asn Asp His Gly Ala Gln Asn Leu Leu Leu Tyr	
140	595 600 605	
141	agt gac cag aag agg tgc tga	1845
142	Ser Asp Gln Lys Arg Cys	

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143          610
145 <210> SEQ ID NO: 2
146 <211> LENGTH: 614
147 <212> TYPE: PRT
148 <213> ORGANISM: Mus sp.
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152 Thr Thr Gly Phe Asn His Ser Ala Cys Ala Thr Lys Lys Leu Leu Trp
153      20          25          30
154 Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu
155      35          40          45
156 Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro
157      50          55          60
158 Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu
159      65          70          75          80
160 Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu
161      85          90          95
162 Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His
163      100         105         110
164 Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro
165      115         120         125
166 Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu
167      130         135         140
168 Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp
169      145         150         155         160
170 Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser
171      165         170         175
172 Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys
173      180         185         190
174 Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala
175      195         200         205
176 Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln
177      210         215         220
178 Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg
179      225         230         235         240
180 Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile
181      245         250         255
182 Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys
183      260         265         270
184 Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp
185      275         280         285
186 Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu
187      290         295         300
188 Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile
189      305         310         315         320
190 Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys
191      325         330         335
192 Phe Ala Gln Asn Ser Ile Gly Asn Thr Thr Arg Thr Ile Arg Leu Arg

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193          340          345          350
194  Lys Lys Glu Glu Val Val Phe Val Tyr Ile Leu Leu Gly Thr Ala Leu
195          355          360          365
196  Met Leu Val Gly Val Leu Val Ala Ala Ala Phe Leu Tyr Trp Tyr Trp
197          370          375          380
198  Ile Glu Val Val Leu Leu Cys Arg Thr Tyr Lys Asn Lys Asp Glu Thr
199          385          390          395          400
200  Leu Gly Asp Lys Lys Glu Phe Asp Ala Phe Val Ser Tyr Ser Asn Trp
201          405          410          415
202  Ser Ser Pro Glu Thr Asp Ala Val Gly Ser Leu Ser Glu Glu His Leu
203          420          425          430
204  Ala Leu Asn Leu Phe Pro Glu Val Leu Glu Asp Thr Tyr Gly Tyr Arg
205          435          440          445
206  Leu Cys Leu Leu Asp Arg Asp Val Thr Pro Gly Gly Val Tyr Ala Asp
207          450          455          460
208  Asp Ile Val Ser Ile Ile Lys Lys Ser Arg Arg Gly Ile Phe Ile Leu
209          465          470          475          480
210  Ser Pro Ser Tyr Leu Asn Gly Pro Arg Val Phe Glu Leu Gln Ala Ala
211          485          490          495
212  Val Asn Leu Ala Leu Val Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys
213          500          505          510
214  Phe Cys Ser Phe Gln Glu Pro Glu Ser Leu Pro Tyr Leu Val Lys Lys
215          515          520          525
216  Ala Leu Arg Val Leu Pro Thr Val Thr Trp Lys Gly Leu Lys Ser Val
217          530          535          540
218  His Ala Ser Ser Arg Phe Trp Thr Gln Ile Arg Tyr His Met Pro Val
219          545          550          555          560
220  Lys Asn Ser Asn Arg Phe Met Phe Asn Gly Leu Arg Ile Phe Leu Lys
221          565          570          575
222  Gly Phe Ser Pro Glu Lys Asp Leu Val Thr Gln Lys Pro Leu Glu Gly
223          580          585          590
224  Met Pro Lys Ser Gly Asn Asp His Gly Ala Gln Asn Leu Leu Leu Tyr
225          595          600          605
226  Ser Asp Gln Lys Arg Cys
227          610

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229 <210> SEQ ID NO: 3

230 <211> LENGTH: 754

231 <212> TYPE: DNA

232 <213> ORGANISM: Homo sapiens

233 <220> FEATURE:

234 <221> NAME/KEY: misc_feature

235 <222> LOCATION: (6)..(8)

236 <223> OTHER INFORMATION: "n" = a, t, c, g

237 <221> NAME/KEY: misc_feature

238 <222> LOCATION: (563)..(563)

239 <223> OTHER INFORMATION: "n" = a, t, c, g

W--> 240 <221> misc_feature

241 <222> LOCATION: (596)..(596)

242 <223> OTHER INFORMATION: "n" = a, t, c, g

RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,7,8,563,596,607,708,729,752

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10737146.raw

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L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:240 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:243 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:246 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:249 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:255 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
L:303 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:0